

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 110392

TO: Rita Mitra

Location: cm1/9b03

Art Unit: 1653

Monday, December 15, 2003

Cas Serial Number: 09/874062

From: Barb O'Bryen

Location: Biotech-Chem Library

CM1-6A05

Phone: 308-4291

BOB

barbara.obryen@uspto.gov

Search Notes	The second secon		
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O'Bryen, Barbara

Fr m:

Mitra, Rita

Sent:

Friday, December 12, 2003 5:05 PM Chan, Christina

T : Cc:

O'Bryen, Barbara

Subj ct:

Frame search request 09/874062

Hi Christina Chan

I need a frame search done foe count Mon. I have spoken to Barbara at STIC, she said it is possible for her to do. Could you please approve this rush request?

Thanks. Rita

Please send the approval directly to Barbara O'Bryen.

I would like to request an expedited sequence search for application 09/874062 because this is an amended case and due this Monday. Please search commercial databases and published patent databases.

Please do only a frame search of amino acid sequence of SEQ ID NO: 3 against nucleic acid databases.

09/874062

SEQ ID NO: 3 against nucleic acid databases (frame Search)

Please print out results.

Thank You.

Rita

Rita Mitra, Ph. D. Examiner Art Unit 1653 CM-1, 9B03 (703)605-1211

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Command line parameters:
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1484
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1...52
| Acganism="Mus musculus"
| mol type="mRNA"
| strain="CSTBL/6J"
| Ab_xref="FANTOM DB:1110054P19"
| Ab_xref="FANTOM DB:1110054P19"
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| About type="whole body"
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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Vokohama Institute; 1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 920)
         Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Ttoh, M., Komoo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Nature 409 (6821), 685-690 (2001)
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Direct Submission
                                                     Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1517-1630 (2000)

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RUL:http://genome.gsc.riken.go.jp,

Adachi, J., Aizawa, K., Atimura, T., Arakawa, T., Carninci, P., Fukuda
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Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
Submission
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
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Email: bento-soaresoulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesia of first strand chordide that was used to prime the synthesia of first strand oDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to identify it as a clone from the normalized brown adipose library cDNA Library Proparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-33, >POLY_A#Simple_repeat 391-516, >(CAG)#Simple_repeat
Seq primer: MI3 Forward
POLYA=Yes:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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UI-R-CN1-clz-a-10-0-UI.sl UI-R-CN1 Rattus norvegicus cDNA clone
UI-R-CN1-clz-a-10-0-UI 3', mRNA sequence.
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                         315 AGGCCCACCTGCTGTGTGTGTGTGTGCATTTCCAGCTGCTGCAGG-----
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Coordinated Laboratory for Computational Genomics

    .725
/organism="Rattus norvegicus"
/mol_type="mRNA"

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Rattus norvegicus
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/ Organisms = "Now Suprems = "And Lype="mRNA"

/ Ab xref="taxon:966"
/ Alone="IMARS:1959821"
/ Libou = "IMARS:1959821"
/ Libou = "IMARS:1959821"
/ Libou = Index = "Index = "I
                                                                                                                                                 BE250684 1302F1 NIH_MGC_17 Homo Bapiens CDNA clone IMAGE:2959821 5',
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11 H-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at: image.llnl.gov
Plate: LLCM52 row: c column: 22
High quality sequence start: 51
High quality sequence stop: 751.
Location/Qualifiers
I. 759
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   4 SerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGlyGlnGluSer
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Matches:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Homo sapiens
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The corresponding plates are R-CNO-BLW, R-CNO-BLD, R-CNO-BLG, R-CNO-BLP, R-CNO-BLR, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, R-CNO-BLL, and R-CNO-BLR, R-CNO-BLL.

This pool represented 5% of the final driver population.

b) a pool of the 28 most abundant clones in the CNO pool corresponding to the following addresses: bkw-a-09-0-UI, bkw-b-109-0-UI, bkx-d-06-0-UI, bkx-d-01-0-UI, bkx-d-01-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, bkx-d-06-0-UI, bkx-d-11-0-UI, bkx-d-01-0-UI, bkx-d-06-0-UI, blx-d-01-0-UI, bla-a-02-0-UI, bla-f-04-0-UI, bla-q-07-0-UI, bla-q-07-0-UI, bla-a-12-0-UI, bla-d-0-0-UI, bla-d-0-UI, bl
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TAG_TISSUE=brown adipose
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67.00%
59.37%
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Best Local Similarity:
Query Match:
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Pred. No.:
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ORIGIN
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/db_xref="taxon:10090"
/clone="UUGC2M0229J04"
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76.80%
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Dunn,D., Aoyagi,A.)

Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TH DNA polymerase and TH polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pw/042 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                      /lab host="E. coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC2M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (female) was obtained from the Jackson
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Matches:
Conservative:
Mismatches:
Indels:
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/strain="C57BL/6J"
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The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

RS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,

Arakawa, T., Bono, H., Carnind, P., Fukuda, S., Fukunishi, Y.,

Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, W., Isawa, M.,

Kasukawa, T., Kato, H., Kawai, J., Kohno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,

Nomura, K., Numazaki, Y., Ohno, M., Okzaki, Y., Okido, T., Owa, C.,

Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sogabe, Y.,

Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sogabe, Y.,

Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,

Shibata, K., Shibata, Y., Yamamura, T., Yasunishi, A., Yoshida, K.,

Yoshino, M., Muramasu, M. and Hayashizaki, Y. Tanaka, T.,

Direct Submission

Submitted (10-JUL-200) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp,, URL:http://genome.gec.riken.go.jp/, Tel:81-45-503-9222,

Parsell 45-503-9216)
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similar to KERATIN ASSOCIATED PROTEIN 4.14 (Homo sapiens)
(SPTR|Q9BYQ6, evidence: FASTY, 71.5%ID, 79.4%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                                          HTC 05-DEC-2002
                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                           Mus musculus adult male tongue CDNA, RIKEN full-length enriched library, clone:2300006N05 product:similar to KERATIN ASSOCIATED PROTEIN 4.14 [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                     604 CGCCCCATCTGCTGCAGCCCAGCTGCTGTGTGTCTAGCTGC 645
                                                                                                                                    181 GlnProSerCysCysArgProAlaCysCysIleSerSerCys 194
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
927/923
10349636
                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                             821 bp
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AK009035.1 GI:12843584
HTC; CAP trapper.
Mus musculus (house mouse)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konoo, H., Adachi, J., Fukuda, S., Alzawa, T., Hara, A., Fukunishi, Y., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bnoo, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchl, P., Lewis, S., Mill, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Loros, F., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wanshizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohteuki, S.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium and the RIKEN Genome Exploration Research
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Nature 409 (6821), 685-690 (2001)
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                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
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Conservative:
Mismatches:
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AK029194
AK029194.1 GI:26081204
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                             x AK009035
                    2.55e-48
810.50
63.93%
56.56%
54.62%
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/(issue_type="rhabdomyosarcoma"
/lab_host="nblub (phage-resistant)"
/clone_lib="NIH MGC_l7"
/clone_lib="NIH MGC_l7"
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Directionally cloned into EcoRI/XhoI sites using the birectionals, cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGGGG; Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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425 TGTCAGCCCAGGTGCTGTATCTCCAGCTGCTGTCAGCCCAGGTGCTGTATCTCCAGCTGC 484
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 495)

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his clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seg primer:
pCMV-M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished
                                                                      |||:::|||
485 TGCCAGCCC-----TGCTGCAGGCCTAGCTGCTGTCAGTCAGCTGCAGCTGC
                                                                                                                                                             CysHisProSerCysCysValSerSerCysArgCysProPheSerCysProThrThrCys
                                            CysLysProSerCysCysGlnThrCysCysArgProSerCysCysIleSerSerCys
                                                                                                                                   175 TyrArgProGlnCysCysGlnProSerCysCysArgProAlaCysCysIleSerSerCys
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Peld 580, D-69120 Heidelberg, Germany
RZPD: IMAG9958C252.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Golbin/showlib.pl.cq1/response7libNos-972 Contact: Ina Rolfs
Din/showlib.pl.cq1/response7libNos-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/ int file
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                Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysArgProSerCysCysIleSerSerCysCysLysProSerCysCysArgThrThrCys 134
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    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL.http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegani,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiwagi,K., Yonada,Y., Ishikawa,T., Ozawa,Y., Tamaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Nature 409 (6821), 685-690 (2001)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310037K05 product:similar to KERATIN ASSOCIATED PROTEIN 4.15 (FRAGMENT) [Homo sapiens], full insert sequence.
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Mismatches:
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Matches:
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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790.00
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105 bp mRNA linear EST 17-DEC-2002
BY723070 RIKEN full-length enriched, 6 days neonate skin Mus
musculus cDNA clone A030010K20 5', mRNA sequence.
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URL.http://genome.gec.riken.go.jp/
Adachi.J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K.,
Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno
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Mammalia; Eutheria;
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/trānalation="MVSSCCGSVCSEEGCSQGCCQPSCCVSSCCRPQCQGSVCCQPTC
CRPSCCISSCCRPSCCRPSCCRPSCCVSSCCRPQCCQSACCQPTCCRPSCCRPSCCIS
SCCQPSCGGSSCCGSCCRPCCRPCCRPCCLRPVCGQVCCQTTCYRPTCVISTCPRP
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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similar to KERATIN ASSOCIATED PROTEIN 4.15 (FRAGMENT)
[Homo sapiens] (SPTR|Q9BYQ5, evidence: FASTY, 70.7%ID,
96.8%length, match=495)"
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/organism="Mus musculus"
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="MG1:1909981"
/db_xref="taxon:10090"
/clone="2310037K05"
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Gaps:
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|db_xref="GI:12844600"
|db_xref="MGI:1923694"
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55. .561
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Mammalish Sufferlish Kodentish Scilitognachi; Muridae; Mutrhae; Mushamalish Sufferlish Schonbach, C. , Guachach, C. , Golobori, T. , Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Guackehoush, J., Schriml, L.M., Kanapin, A., Matada, B. , Golobori, T. , Schriml, L.M., Kanapin, A., Matada, C., Godzik, A., Frazer, K.S., Gaasererland, T. A., Fletcher, C.F., Forrest, J. L. K., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongagaya, M., Matachich, L., Marchiconni, L., McKenzie, L., Muschand, B., Matchiconni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petcovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, I., Yang, I., Wakawa, T., Konno, H., Nakawa, K., Arakawa, T., Konno, H., Nakawa, K., Shirak, K., Shinagawa, R., Yasunish, R., Shara, A., Sakaki, D., Saton, R., Shinagawa, R., Yasunish, A., Sokhino, M., Wasaki, D., Shibata, K., Shinagawa, A., Yasunish, A., Sakai, K., Shinagawa, R., Yasunish, A., Woshino, M., Wasaki, D., Bander, M., Shinagawa, R., Yasunish, A., Woshino, M., Wasaki, D., Bander, M., Wasaki, M., Saka, W., Saka, Yasunish, A., Wasawa, M., Saka, W., Sako, W., Wang, Y., Shinagawa, M., Saka, W., Wang, Y., Shinagawa, 
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                          327 AGCTCCAGCTGCTGTGTTCTAGCTGCTGC---CGCCCCTGCTGCCGCCCTGCTGCTGCTGCAGC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysCysIleSerSerCysCysArgProSerCysCysIleSerSerCysCysLysProSer 158
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                            61 LysProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCys
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                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format squencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inote="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [3], cDNA was GAGAGGAGGAAGGATCCAAGAGCTTTTTTTTTTTTTVN 3'], cDNA was
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      ,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Satio,R., Sakazume,N., Sano,H.,
Saeaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/db_xref="taxon:10090"
/clone="A030010K20"
/tissue_type="6 fays neonate"
/lab_host="DH10B"
/lab_host="DH10B"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                      563 TACCAGCCAACATGTGTCTGTGTGCCTGGCTGTCCCAAGGCTGTGGGTCTAACTGC
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AK003994.1 GI:12834987
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-resegger:riken.go.jp,
VRL:http://genome.gsc.riken.go.jp/
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Akimura,T., Arakawa,T., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nohmura,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/tisasue type="whole body"
/dev_stage="18-day embryo"
/clone_lib="RIKEN full-length enriched, 18-day embryo
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                  Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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/note="unnamed protein product; ULTRA-HIGH SULPHUR KERATIN homolog [Mus musculus] (SPTR|Q64526, evidence: FASTY, 91.2%ID, 98.9%length, match=582) putative"
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/br.xref="GI:12834988"
/db_xref="MGI:1309997"
/translation="MTNSCCSPCCQPICCRTTCWRPSCVTSCCQPSCCG
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|db_xref="MG1:1906631"
|db_xref="taxon:10090"
|clone="1110030N11"
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Punctional annotation of a full-length mouse cDNA collection
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S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Alzawa, K., Akahira, S., Fukunishi, Y.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Hiracka, T., Hori, F., Imotani, K., Ishli, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sagaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tojani, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Toshino, M., Muramatsu, M. and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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further details.
Genome Res. 10 (11), 1757-1771 (2000)
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So (kazakı, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Haseqawa, Y., Nogami, A., Schonbach, C., Osiobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schrim, I.M., Kanapin, A., Matuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Burusic, V., Chothia, C., Gorbani, J. E., Cousins, S., Gassterland, T., Garibold, M., Jackson, I., Gough, J., Karatin, E., Hirokawa, M., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.B., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Percovsky, N., Pilai, K., Pontius, J.U., Qi, D., Ramachandran, S., Randelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Wanshesett, C., Wansiy, Y., Rangil, W., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shangil, Y., Wangari, Y., Zimmer, A., Arakwa, T., Kung, L., Wangere, L., Wahlestedt, C., Wangil, Y., Zimmer, A., Arakwa, T., Kung, Z., Zavolan, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakwa, T., Kuda, S., Hara, A., Hashizume, W., Inotani, K., Shinagawa, A., Yasunishi, A., Sakai, K., Sakai, S., Hara, A., Hashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cons
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9222
Fax: 81-45-503-9226
Email: genome-res@gsc.riken.go.jp,
WL:http://genome-gsc.riken.go.jp,
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Y., Hashizume,M., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibara,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
Submission
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                                     506 CTCAAC---CTGTGCTGCCAGCCTGGCTCTGGACCTGTGACCTGCACAGGACTTGC 562
175 TyrargProGlnCysCysGlnProSerCysCysArgProAlaCysCysIleSerSerCys 194
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus
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SOURCE

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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whole_body"
                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for
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KEYWORDS SOURCE AUTHORS TITLE JOURNAL

MEDLINE PUBMED

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REFERENCE AUTHORS MEDLINE PUBMED

REFERENCE AUTHORS

JOURNAL

TITLE

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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs

IL Nature 420, 563-573 (2002)

E (bases 1 to 963)

E (bases 1 to 963)

E Adachi, J. Alazawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Haradka, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, Y., Owa, C., Nommazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, Y., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, T., Toya, T., Yashino, M., and Hayashizaki, T., Tarai, The Institute of
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62. .565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                             Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110033F04 product:weakly similar to KERATIN ASSOCIATED PROTEIN 4.12 (SIMILAR TO RIKEN CDNA 1110054P19 AK004055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                      CysCysGlnThrThrCysCysArgProSerCysCysIleSerSerCysTyrArgProGln 178
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 970)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagli,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T., Baldarelli,R., Hill,D.D., Bult,C., Hume,D.A.,
Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
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                                                                                                                                                                                                           MetValSerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly 20
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Matches:
Conservative:
Mismatches:
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Mus musculus
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Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kawali, H., Kawasawa, Y., Kedateski, R.M., Kanasa, A., Kurochin, I.V., Lee, Y., Lenhard, B. L., Wing, B.L., Konagaya, A., Kurochin, I.V., Lee, Y., Lenhard, B. L., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Reid, J., Ring, Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.B., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Secou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Taskada, F.R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagiawa, M., Yang, I., Yang, L., Yuan, Z. Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hiozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Tuch, M., Yang, I., Watazaki, A., Yashinaqawa, A., Yashinaya, R., Yashino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length constructional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Exploratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute for First Science of Physical and Chemical Research (RIKEN) 1-7-22 Suehitro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226 Fax: 81-45-503-9226 Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp, Vakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Konno,M., Nawazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Wakai,L., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for trapper-selected cDNAs to prepare full-length cDNA libraries for trapper selected cDNAs to prepare Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RIKEN full-length enriched, 10 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site 1: Sal1; Site 2: BamH1; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
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'dev stage="10 days neonate"
'lab_host="DH10B"
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clone="5530401L02"
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/strain="C57BL/6J"
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                                                                CysLysProSerCysCysArgThrThrCysCysArgProSerCysCysIleSerSerCys 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 ArgProAlaCysCysIleSerSerCysCysHisProSerCysCysValSerSerCysArg 205
Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGGAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 TGTATCTCCAGCTGCTGC---CAGCCCTGCTGCAGGCCTAGCTGCTGTCAGTCCAGCTGC 463
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        Search completed: December 13, 2003, 07:30:04

        Job time: 2165 secs
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Sequence 43, App.

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1484
1 WVSSCCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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SUMMARIES

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Sequence 2, Application US/09874062
Patent No. US20020081607A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Polypeptides and Antibodies
FILE REFERENCE: PT033P1
CURRENT APPLICATION NUMBER: US/09/874,062
CURRENT PILING DATE: 2001-06-06
PRIOR PPLICATION NUMBER: PT7/US00/32462
PRIOR APPLICATION NUMBER: 60/168,229
PRIOR FILING DATE: 1999-12-01
                                                                                                                                                                                                                         Sequence 6114, Ap Sequence 24945, A Sequence 24945, A Sequence 2011, Ap Sequence 2011, Ap Sequence 110244, Sequence 110244, Sequence 110244, Sequence 21990, Ap Sequence 21990, Ap Sequence 21989, A Sequence 273489, Sequence 263173, Sequence 263173, A
                   Sequence 20613, A
Sequence 1, Appli
Sequence 25152, A
Sequence 6, Appli
                                                                                                   Sequence 20464, A
Sequence 20498, A
Sequence 25183, A
Sequence 284090,
Sequence 284090,
Sequence 7, Appli
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US-09-864-761-4747

US-09-864-761-27528

US-09-864-761-27528

US-09-864-761-10890

US-09-864-761-10890

US-09-864-761-10842

3 US-10-027-632-110244

4 US-10-027-632-110244

4 US-10-027-632-110244

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1 US-10-029-386-24902

1 US-10-029-386-24902

1 US-10-029-386-25308

1 US-10-029-154-1390

1 US-10-029-154-1390
3 US-10-120-988-43
3 US-10-029-386-20613
3 US-10-029-386-25152
3 US-10-029-386-25152
3 US-09-950-051-6
3 US-10-029-386-20464
3 US-10-029-386-25183
3 US-10-029-386-25183
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3 US-10-029-386-25183
3 US-09-986-051-7
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US-10-029-366-25198

US-10-027-632-273489

US-10-027-632-273489

US-10-027-632-273489

US-10-027-632-273489

US-10-027-632-273489

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US-10-027-632-273488
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                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 3
SOFTWARB: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1101
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SerSerCysArgCysProPheSerCysProThrThrCysCysArgThrThrCysPhe--- 220
                                                                                                                                                                                                                       ---ThrCysCysArgProSerCysCysIleSerSerCysTyrArgProGlnCysCysGln 181
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206 CAGCCCACCTGCTGCCGTCCCAGCTGCTGTCCCAGCTGCTGTCAGACCACCTGCTGCAGG
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                                                                                                                                                                                       1 MetValSerSerCygCygGlySerValCygSerAspGlnSerCygGlyGlnGlyLeuGly
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                                                                                                                911
169
14
33
38
                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                       US-09-874-062-3 (1-230) x US-10-120-988-43 (1-911)
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SEQ ID NO 43
LENGTH: 911
                                                                                                               4.1e-76
1053.00
72.05%
66.54%
                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                FEATURE:

NAME/KEY: CDS

LOCATION: (38)..(760)

US-10-120-988-43
                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                         Alignment Scores:
Pred. No.:
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                                                                                                                        CAGGAGAGCTGCTGCCGCCCCAGCTGCTGCCAGACCACCTGCTGCTGCAGGACCACCTGCTGC 156
                                                                                                        GlnGluSerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCys 40
                                                                                                                                                                         80
                                                                                                                                                                                                        AAACCCAGCTGCTGCCTGACCACCTGCTGCAGCACCACCTGCTGCCGCCCCAGCTGCTGC
                                                                        LysProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/10120988
Publication No. US2030219745A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Control
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT FILING DATE: 2002-04-11
  1101
230
0
0
0
  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                         US-09-874-062-3 (1-230) x US-09-874-062-2 (1-1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.24e-110
1484.00
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              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-120-988-43
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 ---CAGTGCTGCCAGACCACCTGCTGC 423
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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                  Sequence 1, Application US/10294804

Publication No. US20030133948A1

GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
ITILE OF INVENTION: Methods to Inhibit or En;
ITILE OF INVENTION: Methods to Inhibit or En;
ITILE OF INVENTION: Methods to Inhibit or En;
ITILE OF INVENTION: WUMBER: US/10/294,804

CURRENT RPLICATION NUMBER: US/09/410,399

PRIOR APPLICATION NUMBER: US/09/410,399

PRIOR APPLICATION NUMBER: US/09/410,399

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN VOIT: 2.0
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379 GTGTCCAGCTGCTGCAGACCC-
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733.00
57.32%
51.05%
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Best Local Similarity:
Query Match:
D8:
                                                                                                                         US-10-294-804-1/C
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                                                                                                                                                                                                                                                                                                                               TYPE: DNA

OCHAEN INFORMATION: MAP TO AC006070.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: SYPET HUMAN HIT: BELSOG64.1, EVALUE 5.50e+00

OTHER INFORMATION: SYPET HUMAN HIT: P26371, EVALUE 5.50e+00

OTHER INFORMATION: NT HIT: 9114210533, EVALUE 0.00e+00
                                                           Sequence 200613, Application US/10029386
Fublication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, blarton G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NU;
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: BXPRESSION ANALYSIS TWO
TITLE OF INVENTION: AND SERVED SINGLE EXON NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOUTHARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 20613
 716 TCCACCTGTCCCCGCCCCTTGTGCTGTGCCTCCTTGCTGC
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
DB:
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US-10-029-386-20613
                                                  -10-029-386-20613
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TITLE OF INVENTION: GENES AND THE PHYSICS OF THE DNA DOUBLE HELIX.
TITLE OF INVENTION: FORMULATION OF A PHYSICS-BASED GENE IDENTIFICATION
TITLE OF INVENTION: FORMULATION OF A PHYSICS-BASED GENE IDENTIFICATION
TITLE OF INVENTION: EUKARYOTIC GENOMES
FILE REFERENCE: 03495-0209-00000
CURRENT PAPLICATION NUMBER: US/09/950,051
CURRENT PILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/232,146
PRIOR FILING DATE: 2000-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                             727 IGCICTGAGGAITCCICTICATGCIGCCAGCAGTCTAGCIGCCAGCCGGCTTGCTGCACC
                                     CysArgProAlaCysCysIleSerSerCysCysHisProSerCysCysValSerSerCys
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----SerCysCysArgThrThrCys
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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ORGANISM: Homo sapiens
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US-09-950-051-6
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                           172 SerSerCysTyrArgProGlnCysCysGlnProSerCysCysArgProAlaCysCysIle 191
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                                                                                                                                                                                                                                                                                             212 ThrThrCysCysArgThrThrCysPheHisProIleCysCysGlySerSerCysCys 230
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OTHER INFORMATION: EST HUMAN HIT: BF057518.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: AL163300.2, EVALUE 0.00e+00
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NU;
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NU;
TITLE OF INVENTION: BXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Best Local Similarity
Query Match:
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US-10-029-386-25152
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LENGTH: 1229
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Pred. No.:
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                                                         N: EXPRESSED IN BRAIN, SIGNAL = 1.6
N: EXPRESSED IN HELA, SIGNAL = 2.7
N: EXPRESSED IN HELA, SIGNAL = 1.4
N: EXPRESSED IN LUNG, SIGNAL = 1.5
N: EXPRESSED IN HEART, SIGNAL = 1.7
N: EXPRESSED IN HEART, SIGNAL = 1.7
N: TALISSED IN BONE MARROW, SIGNAL = 1.7
N: MY HIT: ALIS3100.2, EVALUE 1.00e-123
N: SMISSPROT HIT: P08131, EVALUE 2.00e-04
N: EST_HUMAN HIT: BF057518.1, EVALUE 1.00e-120
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Matches:
Conservative:
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Indels:
                                               TO AJ011930.1
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661.50
51.90%
40.83%
TYPE: DNA
PREATURE:
OTHER INFORMATION: MAP TOTHER INFORMATION: EXPREOTHER INFORMATION: EXIS
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMINGAR: 105/10/29,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 20464
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 SerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCysArgPro
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EXON NUCLEIC ACID PROBES USEFUL FOR
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292 TGTGTCCCACCTGCTCTGAGGATTCCTTCATGCTGCCAGCAGTCTAGCTGCCAGCA 233
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EXPRESSED IN HELA, SIGNAL = 0.84

NT HIT: ALIGA3300.2, EVALUE 0.000+00

EST HUMAN HIT: BF057369.1, EVALUE 0.000+00

SWISSPROT HIT: Q01042, EVALUE 3.900-02
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HARSEL, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE REPERENCE: AEOMICA-x-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25183
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Conservative:
Mismatches:
Indels:
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643.50
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Publication No. US20030194704A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Penn, Sharion G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMBAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FILE REPRENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

LENGTH: 1002
                         1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysGlySerValCysSerAsp-----GlnSerCysGlyGlnGlyLeuGlyGln 21
       -----IleSerSerCysCysHisPro---SerCysCysValSerSerCysArgCys
                                                                        207 ProPheSerCysProThrThrCysCysArgThrThrCysPheHisProlleCysCysGly
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EXPRESSED IN HELA, SIGNAL = 1.5
EXPRESSED IN BONE MARROW, SIGNAL = 1.4
EXPRESSED IN LUNG, SIGNAL = 1.2
SWISSEROT HIT: 0.7560, EVALUE 7.40e-01
EST HUMAN HIT: BF057369, I, EVALUE 0.00e+00
NT HIT: AL163300.2, EVALUE 0.00e+00
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Conservative:
Mismatches:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: MAP TO AJOI1930.1
OTHER INFORMATION: EXPRESSED IN ADULT I.
OTHER INFORMATION: EXPRESSED IN HELA, E.
OTHER INFORMATION: EXPRESSED IN LUNG, OTHER INFORMATION: EXPRESSED IN LUNG, OTHER INFORMATION: EXPRESSED IN LUNG, OTHER INFORMATION: SWISSPROT HIT: 075(); OTHER INFORMATION: SWISSPROT HIT: BF0.
US-10-029-386-20498
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Best Local Similarity:
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                                                                                    CysCysIleSerSerCysCysLysProSerCysCysLeuThrThrCysCysArgThrThr 73
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                      ---GlnSerCysGlyGlnGlyLeuGlyGln 21
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Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.18
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                     CysGlySerValCysSerAsp-
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR ELLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-30
PRIOR PLING DATE: 1999-09-30
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dy 55 CyalleSerSerCysCysLysProSerCysCysLeuThrThrCysCys 70	71 271	97 5	99 CyeCyeArgThrThrCyeCyeArgProSerCysCysIle	113 SerCysCysArgProSerCysCysIleSerSerCysCysLysProSerCysArgThr	133 ThrCysCysArgProSerCysCysIle 133 ThrCysCysArgPro	Qy 142 SerSerCysGysAxgProSerCysGysCysIleSerSerCysGysCysGln 161	171	185CyaArgProAlaCysCysIleSerSerCysHisProSer 750 TCAGGCTGCATCAGCTCCTGCTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCT	199	Qy 219 CysPheHisProlleCysCysGlySerSerCys 229	RESULT 12 US-09-950-051-7/c	; Sequence ', Application US/0950031. ; Publication No. US20030129594Al ; GENERAL INFORMATION: APPLICANT: YERANIAN: EDOUARD ; TITLE OF INVENTION: GENES AND THE PHYSICS OF THE DNA DOUBLE HELIX. ; TITLE OF INVENTION: FORMULATION OF A PHYSICS-BASED GENE IDENTIFICATION ; TITLE OF INVENTION: PRICAPPLY OF A PHYSICS-BASED GENE IDENTIFICATION ; TITLE OF INVENTION: PRICAPPLY OF A PHYSICS-BASED GENE IDENTIFICATION ; TITLE OF INVENTION: PRICAPPLY OF GENES IN	CURRENT APPLICATION NUMBER: US/09/950,051	CORRENT FILLING DATE: 2001-09-12 PRIOR APPLICATION UNMER: 60/232,146 PRIOR FILING DATE: 2000-09-13 NUMBER OF SEQ ID NOS: 9 NUMBER OF SEQ ID NOS: 9	1800	; ORGANISM: Homo sapiens . US-09-950-051-7 Alignment Scores:
Oy 162 ThrThrCysCysArgPro	Oy 171 IleserSerCygTyrArgProGlnCygCygGlnProSerCyg	Qy 185	OY 199 CYSCYSVALSerSerCysArgCysProPheSerCysProThrThrCysCysArgThrThr 218	Qy 219 CysPheHisProlleCysCysGlySerSerCys 229	RESULT 11 US-10-027-632-284090 ; Sequence 284090, Application US/10027632 ; GENERAL INFORMATION:	<pre>; APPLICANT: Wang, David G. ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide ; TITLE OF INVENTION: Polymorphisms in the Human Genome : FILE REFERENCE: 108827.129</pre>		PRIOR PRIOR	APPLICATION NUM FILING DATE: 19 APPLICATION NUM FILING DATE: 19	NUMBE SOFTW SEQ ID LENG	; TYPE: DNA ; ORGANISM: Human US-10-027-632-284090	Alignment Scores: 5.48e-41 Length: 898 Pred. No.: 615.50 Matches: 107 Score: 615.50 Matches: 33 Percent Similarity: 48.11 Conservative: 33 Guery Match: 14.48 Indels: 71 DB: 14.48 Gaps: 10	US-09-874-062-3 (1-230) x US-10-027-632-284090 (1-898)	Qy 4 SerCysCySGlySerValCysSerAspGlnSerCysGlyGlnGlyLeu	Qy 20GlyGlnGluSerCysCysAxgProSerCysClnThrThrCysCysArg 36	Qy 37 ThrThrCysCysArgProSerCysCysIleSerSerCysCysArgProSerCys 54 :::::: :::

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COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
OTHER INFORMATION: EXPRESSED IN MULT LIVER, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN PACKING, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PILLING DATE: 2000-10-04
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Sequence 6314, Application US/09864761

Sequence 6314, Application US/09864761

Sequence 6314, Application US/09864761

Sequence 6314, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL. FITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-K-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR FILING DATE: 2000-02-04
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          Length:
Matches:
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GENERAL INFORMATION:

APPLICANT: Penn. Sharron G.

APPLICANT: APICANT: BAIK, DAYIG R.

APPLICANT: HANG, DAYIG R.

APPLICANT: HANG, DAYIG R.

APPLICANT: HANG, DAYIG R.

APPLICANT: HANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR STATE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FOR EXPRESSION ANALYSIS BY MICROARRAY FILE OF INVENTION UNMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-08-23

PRIOR FILING DATE: 2000-08-23

PRIOR PELING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 2001-01-30

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Patent No. US20020048763A1
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: HORAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILLE REFERENCE: AECMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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              SerCysCysIleSerSerCysCysLysProSerCysCysArgThrThrCysCysArgPro
                                  MAP TO AP001067.1

EXPRESSED IN HELA, SIGNAL = 0.25

EST HUMAN HIT: BF057518.1, EVALUE 4.00e-62

SMISSPROT HIT: 075690, EVALUE 1.00e-04

NT HIT: AL163300.2, EVALUE 0.00e+00
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Matches:
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CTHER INFORMATION: EXPRESSED IN BT44, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN FTAL LIVER, SIGNAL = 1.9

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OTHER INFORMATION: EXPRESSED IN BOUL MARROW, SIGNAL = 2.0

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.0

OTHER INFORMATION: EXPRESSED IN HELLOW, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HELLOW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5

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PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR PLING DATE: 2001-01-30

PRIOR PELING DATE: 2000-02-11

PRIOR PLILING DATE: 2000-06-21

PRIOR PLILING DATE: 2000-06-30

PRIOR PLILING DATE: 2000-06-30

PRIOR PRILING DATE: 2000-06-30

PRIOR PRILING DATE: 2000-06-30

PRIOR PRILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

SEQ ID NO 4474
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Job time : 338 secs
                  408
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115, Appl 115, Appl 115, Appl 116, Appl 117, A

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Sequence 15, Appl
Sequence 93, Appl
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Fatent No. 594676

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Belman, Isidore S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Immediate Early Protein Prom Kaposi's
TITLE OF INVENTION: Eacoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
TITLE OF US. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,678
.er: 0575/52268/JPW/MSC/SKS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
US-08-910-647-1
US-09-620-925-1
US-07-884-811-15
US-07-884-811-15
US-08-194-088-15
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US-09-491-315C-7
US-09-521-511C-10
US-09-521-511C-10
US-09-531-37
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
    FILING DATE:
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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US-09-298-568-1

US-09-410-399-1

US-08-770-379-20

US-09-23-31A-20

US-09-23-31A-20

US-09-249-585A-2

US-09-410-399-3

US-09-050-863-2

US-09-130-114-1

US-09-647-344A-14
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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                                                              APPLICANT: Kieff, Eliott D.
APPLICANT: Kieff, Eliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Waye, Kenneth M.
TITLE OF INVENTION: FHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT PELLING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
SARLIER PILING DATE: 1998-11-19
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGlyGlnGlu 22
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Matches:
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Sequence 1, Application US/09298568
Patent No. 6322792
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Kaposi's
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) FEATURE:
     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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733.00
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51.05%
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                                                                                                                                                    TOPOLOGY: linear
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US-09-298-568-1/C
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                                                                                                                        212 ThrThrCysCysArgThrThrCysPheHisProlleCysCysCysGlySerCysCys
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                                                                                          TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: 2
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Mismatches:
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1185 Avenue of the Americas
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FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                      Sequence 20, Application US/08770379
Patent No. 5849564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTOMNEY AGENT INFORMATION:
NAME: White, John P.
REGISTATION UNDMER: 28,678
REFERENCE/DOCKET UNDMER: 52347
TELECOMMUNICATION INFORMATION:
TELEPAK: (212) 278-0400
TELEPAK: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               APPLICANT: Bohenzky, Roy A. APPLICANT: Russo, James J. Sabricant: Edelman, Isidore S. APPLICANT: Moore, Patrick S.
                                                                                                                                                                                                                                                                                           Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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57.32%
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Best Local Similarity:
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Pred. No.:
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US-08-770-379-20
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 GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA FILE REPERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 SerSerCysCysLysProSer---CysCysArgThrThrCysCysArgProSerCysCys 140
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                                                                      1511 GGCTCCTGCTGTTGTGGCTCCTGCAGGGCTCCTGCTGCTGTGGCTCCTGCTGTTGT 1455
                                  212 ThrThrCysCygArgThrThrCygPheHisProlleCysCysGlySerSerCysCyg 230
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Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
LENGTH: 3489
                                                                                                                                               Sequence 1, Application US/09410399
Patent No. 6482587
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Best Local Similarity:
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Conservative:
Mismatches:
Indels:
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REFERENCE/DOCKET NUMBER: 451E;
TELECHUNICATION INFORMATION:
TELEPHONE: (212) 249-0400
TELEPKX: (212) 391-0525;
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
TYPE: NUCleic acid
STRANDEDNESS: double
TYPE: NUCleic acid
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
TOPOLOGY: linear
JOPOLOGY: linear
JC-08-757-669A-20
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Best Local Similarity:
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US-09-230-371A-20
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DB:
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| Sequence 20, Application US/08757669A
| Sequence 20, Application US/08757669A
| Patent No. 6183751
| GENERAL INFORMATION:
| APPLICANT: Chang, Yuan
| APPLICANT: Bohenzky, Roy A. APPLICANT: Bohenzky, Roy A. APPLICANT: Bohenzky, Roy A. APPLICANT: Moore, Patrick S. TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
| TITLE OF INVENTION: SEQUENCES AND USES THEREOF |
| NUMBER OF SEQUENCES: 20 |
| CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: |
| CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESPONDENCE ADDRESS: | CORRESP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
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1185 Avenue of the Americas
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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CLASSIFICATION: 424
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STATE: New York
COUNTRY: U.S.A.
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ORGANISM: Epstein Barr Virus
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48.79%
44.76%
29.99%
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COTHER INFORMATION: coding US-09-249-585A-2
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Best Local Similarity:
Query Match:
DB:
                                                                                                           RESULT 7
US-09-249-585A-2/c
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APPLICANT: Bohenzky, Roy A
APPLICANT: Buttenzky, Roy A
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Red J
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR PAPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
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Matches:
Conservative:
Mismatches:
Indels:
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Sequence 20, Application US/09230371A Patent No. 6348586 GENERAL INFORMATION:
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733.00
57.32%
51.05%
49.39%
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Best Local Similarity:
Query Match:
DB:
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US-09-230-371A-20
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Pred. No.:
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192 SerSerCysCysHisProSerCysCysValSerSerCysArgCysProPheSerCysPro 211
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TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF INTLE REFERENCE 106.7/D0905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
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Conservative:
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121 IleSerSerCys	ON 212 THTHICKYSC/PACETOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Pred. No.: 1.96e-22 Length: 2580
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APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Silva. Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
STREET: 4 Embarcadero Center, Suite 3400
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                    ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
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SEQUENCE DESCRIPTION: SEQ ID
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TYPE: nucleic acid
STRANDEDNESS: unknown
                       CITY: San Francisco
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                                                                       COUNTRY: USA
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Best Local Similarity:
                                                   STATE: CA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
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Patent No. 6316223
GENERAL INFORMATION:
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Payan, Don
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                         Percent Similarity:
Best Local Similarity:
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US-09-359-081-2/c
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                          TOPOLOGY:
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ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUW TYPE: Flogpy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7999 rccccrccrccrccrccrcrr 8022
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NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
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CITY: Emeryville
THATE: California
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Mismatches:
Indels:
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Matches:
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REFERENCE/DOCKET NUMBER: 121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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83 SerCysCysArgProSerCysCysIleSerSerCysCysLysProSerCysCysArgThr 102
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Patent No. 5316921
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
FILING DATE: 19920518
CLASSIFICATION NUMBER: SAPPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 ThrThrCysCysArgThrThrCys 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                             103 ThrCysCysArgProSerCys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3
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ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
                                                                             Sequence 1, Application US/09620925
Patent No. 6468986
GENERAL INPORMATION:
APPLICANT: Zuckermann et al
TITLE OF INVENTION: Compositions and Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-874-062-3 (1-230) x US-09-620-925-1 (1-9600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FULITE, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
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                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
      717 TCCCGCTCCTGCTCCTGT 694
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TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                     CITY: Emeryville
STATE: California
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48.79%
44.76%
29.99%
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Best Local Similarity:
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                                           RESULT 14
US-09-620-925-1/c
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Matches:
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Mismatches:
Indels:
Gaps:
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445.00
48.79%
44.76%
29.99%
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
US-07-884-811-15
                                                                                          Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                       Alignment Scores:
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Search completed: December 13, 2003, 07:31:59 Job time : 115 secs

Run on:

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December 13, 2003, 04:44:18 ; Search time 283 Seconds (without alignments) 2193.890 Million cell updates/sec
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| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
| S1DS1/gcgdata/geneseq-geneseqn-emb1/NA1980.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA20018.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA20018.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA20018.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA20018.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*
| S1DS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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                                                                                                                                                                                                                                                                                                                                                             MVSSCCGSVCSDQSCGQGLG......PTTCCRTTCFHPICCGSSCC 230
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
                                                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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7.0
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Xgapop 10.0 , Xgapext C
Ygapop 10.0 , Ygapext C
Fgapop 6.0 , Fgapext 7
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Maximum DB seq length: 200000000
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Perfect score:
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and is derived by analysis of the total score distribution.

t Query Score Match Length DB 1	484 100. 9.5 82.	1218.5 82.1 627 23	1053 /1:0 911 25 944.5 63.6 1851 22	944.5 63.6 1851 22	, /6/ 51./ 1851 22 8 767 51.7 1851 22	9 733 49.4 3489 21	0 733 49.4 3489 22 1 733 49.4 3489 24	11 733 49.4 3489 24 12 733 49.4 32207 20	733 49.4 137507 19	4 666.5 44.9 1980 24 E 603 40 6 410 22	15 603 40.6 410 22 16 603 40.6 1800 24	7 602.5 40.6 478 22	18 602.5 40.6 478 22 19 602.5 40.6 478 22	20 602.5 40.6 478 22	21 602.5 40.6 478 22 22 602.5 40.6 478 22	23 602.5 40.6 478 23	24 602.5 40.6 478 24 25 601 40 5 1974 22	6 601 40.5 1974 22	7 601 40.5 1974 22	8 601 40.5 1974 22 9 601 40.5 1974 22	0 601 40.5 1974 22	1 601 40.5 1974 22 2 601 40.5 1974 22	3 601 40.5 1974 23	4 601 40.5 1974 24 5 600.5 40.5 1067 24	6 574 38.7 489 22	7 5/4 38.7 489 22 8 574 38.7 489 22	9 574 38.7 489 22	0 5/4 38.7 489 23 1 574 38.7 489 24	2 570.5 38.4 461 22	3 570.5 38.4 461 22 4 570.5 38.4 461 22	5 - 570.5 38.4 461 22	ALIGNMENTS	RESULT 1	AAD06303 ID AAD06303 standard; CDNA; 1101 BP. xx	AC AAD06303;	XX DT 10-AUG-2001 (first entry)	XX DE Human cDNA clone HWHQC55 encoding FDCD-containing
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disulfide core domain (PDCD)-containing protein. FDCD sequences are used to prevent, treat or ameliorate skin disorders such as congenital disorders e.g. moles, freckles and haemanglomas as well as integumentary tumours (keratosis, basal cell carinoma, malignant melanoma), injuries and inflammation of the skin, atherosclerosis, urticaria, eczema, photosensliviviy, autoimmune disorders (lupus crythematosus, scleroderma), keloids, striae, erythema, petechiae, purpura and xanthelasma. They are also used in the diagnosis and treatment of diseases and disorders of hair and epithelium, cutoimmune diseases (e.g. rheumatoid arthritis), hyperproliferative disorders (e.g. cardiac arrest), cardiovascular disorders (e.g. cardiac arrests), cerebrovascular disorders (e.g. cardiac arrests), preventoular disorders (e.g. cardiac arrests), preventoular disorders (e.g. cardiac arrests), preventoular disorders (e.g. containing proteins are used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. They are used in chamosing a pathological condition or susceptibility to a pathological condition. The antibodies to protein are used in alleviating
                 stria; erythema; petechia; purpura; xanthelasma; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebral ischaemia; neoplasm; angiogenesis; nervous system disorder; Alzhaimer's disease; infection; ocular disorder; corneal infection; clone HWHQC55; ds.
erythematosus; scleroderma; keloid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
                                                                                                                                                                                                                                                     "Human four disulfide core domain (FDCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Four disulfide core domains (FDCD) containing polypeptide and its polynucleotide are used to prevent, treat or ameliorate a medical condition associated with FDCD e.g. skin disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is human cDNA clone HWHQC55 encoding four
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                                                                                                                                                                                       Location/Qualifiers 37...729
eczema; autoimmune disorder; lupus
                                                                                                                                                                                                                                                  /product= "Human to
containing protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 229; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2000; 2000WO-US32462.
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Sequence 1101 BP; 220 A; 343 C; 231 G; 307 T; 0 other 1101 230 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: .57e-60 1484.00 100.00% 100.00% 100.00% Similarity: Percent Similarity: Best Local S Query Match:

US-09-874-062-3 (1-230) x AAD06303 (1-1101)

12-SEP-2002.

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                                                                                      97 CAGGAGAGCTGCTGCCGCCCCAGCTGCTGCTGCCAGACCTGCTGCAGGACCACCTGCTGC 156
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                  37 ATGGTCAGCTCCTGCTGTGGCTCTGTCTGTCTGACCAGAGCTGTGGTCAAGGTCTGGC
                                                        GlnGluSerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCys
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 MetValSerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly
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Specification, but was obtained in electronic format directly from WIPO
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                                                                              Ren
                                                                                                                                                           New polynucleotides comprising sequences assembled from expressed aggenere tags (ESTS), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                             Zhao QA, ]
Ghosh M:
                                                                                                                                                                                                                       Claim 1; SEQ ID NO 814; 1012pp + Sequence Listing; English.
                                                                            Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zl
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z,
Wehrman T, Wang J, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 CAGGAGAGCTGCTGCCGCCCAGCTGCTGCCAG------
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1195
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Matches:
Conservative:
Mismatches:
Indels:
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1229.50
84.78
84.78
82.85
            05-MAR-2002; 2002WO-US05095
                               05-MAR-2001; 2001US-0799451
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Best Local Similarity:
                                                       (HYSE-) HYSEQ INC
                                                                                                                                       P-PSDB; ABP69715
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder,
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BP

ABX70816 standard; cDNA; 911

ABX7081 RESULT

(first entry)

05-MAR-2003

ABX70816;

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a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protes expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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194
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Mismatches:
Indels:
Gaps:
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Matches:
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1218.50
84.35$
84.35$
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This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, anyotrophic lateral sclerosis; neurodegenerative diseases (e.g. parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. obserporosis; osteoproteis); nechanical and traumante disorders (e.g. and thrombocytopaenia); wounds, ulcers, burns; bone disorders (e.g. onteoprorosis; osteoprathritis); mechanical and traumante disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic stroke, head trauma); cancer and tumours; and inflammatory disease (e.g. tamenophila); cancer and tumours; and inflammatory disease (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as allergic shock, crohn's disease, anaphylaxis). The protein may also hortythms or circadian cycles of rhythms. The protein may also chave proliferation/differentiation, stem cell growth factor, have proliferation/differentiation, stem cell growth factor, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, chemotactic and expressing recombinant protein for analysis. The invention are useful for expressing recombinant protein for analysis. The invention, this sequence is an expressed sequence tag (EST) and was identified the useful consing subtractive hybridisation.
                                                                                                                                                                                                           Huntington's disease; amyotrophic lateral sclerosis; haemophilia; neurodegenerative disease; Parkinson's disease. Altheimer's disease, autoimmure disease; systemic lupus erythematosus; rheumatoid arthritis; insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound; ulcer; burn; born dissorder; osteoporosis; osteoarthritis; stroke; coagulation disorder; osteoporosis; osteoarthritis; stroke; coagulation disorder; cancer; tumour; inflammatory disease; asthma; septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic; differentiation; stem cell growth factor; haematopoiesis; chemotactic; haemostatic; antinflammatory; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptide useful for treating neurodegenerative diseases, myeloid or lymphoid cell disorders, bone disorders, mechanical and traumatic disorders, coagulation disorders, and inflammatory diseases
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Drmanac RT;
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Wang D,
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Xue AJ, Yang Y, Wehrman T, Wang J,
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                                                                                                                                          Novel human cDNA sequence #41
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ValSerSerCysArgCysProPheSerCysProThrThrCysCysArgThrThrCysPhe

GTGTCCAGCTGCCGCTGCCCTTTCAGCTGCCCGACCTGCTGTGTAGAACAACCTGCTTC

HisProlleCysCysGlySerSerCysCys 230

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Human polynucleotide SEQ ID NO 680.
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                                                     Homo sapiens.
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          G; 211 T; 0 other;
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW7832-AAM88302) that exhibit activity elating to erytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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gene therapy;
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Human, cytokine, cell proliferation, cell differentiation, gene the vaccine, peptide therapy, stem cell growth factor; haematopolesis, tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
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27-APR-2000; 2000US-0566875.
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01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
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Wang ZW;
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Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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R, Wang ZW;
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Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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                                                                                                          127 ProSerCysCysArgThrThr---
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20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-052325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-065351.
30-OCT-2000; 2000US-063325.
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Indels:
                                                Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
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                                                                                                                                                                                                       The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
     TGCCAGCCTTGCTGCCACCCAACATGCTGTCAAACCATTTGTAGATCCACCTGCTGCCAA 1596
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                                                                                                                                                                       ProAlaCysCysIleSerSerCysCysHisProSerCysCysValSerSerCysArgCys 206
                                                           ProSerCysCys11eSerSerCysTyrArgProGlnCysCysGlnProSerCysCysArg 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
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                                                                                                                                                                                    latency-associated nuclear antigen; LANA; gamma-2 herpes virus;
Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;
Kaposi's sarcoma; primary effusion lymphoma; PEL;
human immunodeficiency virus; HIV; multicentric Castleman's disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary Effusion Lymphoma
                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
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/note= "nuclear localisation signal, NLS"
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                                                                                                                                                sarcoma-associated herpesvirus LANA gene.
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P-PSDB; AAY96255
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with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation.
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Human herpesvirus 8.
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                                                                                                                                                                                                                                                                                                                                                                            protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Kaposi's sarcoma associated herpesvirus (human herpesvirus 8) latency-associated nuclear
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                                                                                                                                                                                                                                                                                                                                                                    invention provides a composition comprising nucleic acid, histone H1
Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus B; KSHV; latency-associated nuclear antigen; LANA; ds.
                                                                                                                                                                                                                                                                                               composition for use in gene therapy comprises an expression vector at includes a nucleic acid sequence encoding a nucleic acid binding
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                                              Kaposi's sarcoma associated herpesvirus
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/product= "LANA protein"
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The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigen) of 3489 base pairs (see ABA93487, S1) expressed in the cell, and the rhadinoviral sequence RVCAE (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2) present in the plasmid. Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having (S2) as a cis-acting and maintenance sequence in the DNA. (A) is particularly used in gene therapy (or other gene transfer applications) that uses mammalian cells in which LANA is expressed. (A) improves persistence of gene therapy vectors in cells. The present sequence encodes Kaposi's sarcoma-associated herpesvirus (KSHV, also called human herpesvirus 8) LANA protein, which is used in the exemplification of the
                            6; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
                            Claim 1;
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Sequence 3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 other;

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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, CRF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF67 which encodes immediate early protein (IRP), K14 which encodes (X-2 (Y-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGARAT, K15. KSHV is a new human the encodes tegument protein/FGARAT, K15. KSHV is a new human in the encodes tegument protein/FGARAT, K15. KSHV is a new human const common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
                                                                                                                                                                                                                                                  Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2;
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                      212 ThrThrCysCysArgThrThrCysPheHisProllsCysCysGlySerSerCysCys 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaposi's sarcoma-associated herpes virus nucleic acid - encodes di:hydro:folate reductase and is useful for treatment, prophylaxis or diagnosis of Kaposi's sarcoma
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                                                                                                                                                                                                                                                                                                                           v-adh; G-protein coupled receptor; FGARAT; ds.
                                                                                                                                                                                                                  KSHV LUR DNA (nucleotides 105, 301-137, 507).
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                                                                                                                                                                                                                                                                                                                                                                 Kaposi's sarcoma-associated herpesvirus.
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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known sas human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHV polyapptides selected from: (a) viral macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6); (c) viral IRF i; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                            Η
                                        /product= macrophage inflammatory protein complement (27137..27424)
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'product= interferon regulatory factor
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complement (123808..127296)
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                                                                                                                                                                                                                                                                                                                                                                     /product= glycoprotein X complement (93636..94127)
                complement (21548..21832)
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complement (58976..60175)
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complement (69412..69915)
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complement (88410..88910)
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'product = interleukin 6
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                                                                           42 ProSerCysCysIleSerSerCysCysArgProSerCysCysIleSerCysCysLys 61
                                                                                                                                        62 ProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCysIle 81
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                 SerCysCysArg---ProSerCysCysGlnThrThrCysCysArgThrThrCysCysArg 41
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complement (17261..17875)
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1142..2794
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detecting HHVB, specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHVB infections can be treated with antiennse or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHVB infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHVB may be implicated in many other lymphoproliferative diseases and HHVB may be implicated in many splenomegaly and mycosis fungoides. Cells and animals containing the uncleic acid are useful for drug screening. HHVB-derived peptides can be used as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine
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                                                                                                                                                                                                                 the immune status of a patient infected with HIV. HHVB derived protein viral MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as containing
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967 AGCTCCTGCACGCCCTCGTGCTGCCAGCAGTCTAGCTGCCAGCTGGCTTGCTGTGCCTCC 1026
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125786 GGCTCCTGCTGTTGTGGCCTCCTGCAGGGCTCCTGCTGTGTGCTCCTGCTGTTGT 125842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying genes based on structural properties of a DNA double-helix for identification and discovery of new genes in various eukaryotic genomes, comprises analysing stability curves for the detection of
                                                                                                                                                                                                                                                                                                                                                                 Physics-based gene identification method, novel gene sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Physics-based gene identification method; DNA double-helix; helix-coil transition; DNA stability; sequence analysis; ds
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                                                                                                                                                                   standard; DNA; 1980
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1147 TCAGCTTGCTGCTGCACCTCCCCCTGCCAGCAGGCCTGCTGTGTGCCCATCTGCTGCAAG 1206
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                                                                                                                                                                                                                                                                                                                                                                          -----ProThrThrCysCysArgThr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerCysCysLysProSerCysCysGlnThrThrCysCysArgProSerCysCys--- 170
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                                                                                                                 ProSerCysCysIleSerSerCysCysArgProSerCysCysIleSerSerCysCysLys 96
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                                                63 SerCysCysLeu-----ThrThrCysCysArgThrThrCysArg
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uncleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activities; including cytokine, cell proliferation or cell immunomodulatory activity; tissue growth activity; chaminomodulatory activity; activin. or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or Ingand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders (e.g., myeloid or lymphoid cell cancers), chronic inflammatory conditions (e.g., asthma or arthritis), crepair or nucleic acids encoding them) may be used to promote wound respair growth. Polypeptides may be used in the treatment of viral, tenain definal infections in addition to immune disorders to promote cell cultures to promote cell growth. For example, such polypeptides may be used to neuroephrhalial cells and man and activity may be used in cell cultures to summan and activity may be used to neuroephrhalial cells and an uncaparted and activity may be used to neuroephrhalial cells and an an activity may be used to neuroephrhalial cells and an activity may be used to neuroephrhalial cells and an activity may be used to neuroephrhalial cells and an activit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ins and DNA encoding sequences useful for preventing, ameliorating a medical condition in a mammalian subject
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antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 977; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                    05-PEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                      WO200157188-A2.
                                                       Homo sapiens.
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Matches: Conservative: Mismatches: Indels:

603.00 80.95\$ 73.81\$ 40.63\$

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

3.71e-20

Gaps:

US-09-874-062-3 (1-230) x ABA09521 (1-410)

Search completed: December 13, 2003, 05:52:29 Job time : 338 secs

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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/08FTQ spool/USO8914062/runat 12122003 171322 24931/app_guery.fasta_1.391
-Q=/cgn2 1/08FTQ spool/USO8914062/runat 12122003 171322 24931/app_guery.fasta_1.391
-Q=/cgn2 1/08FTQ spool/USO8914062-rrage -MINMATCH=0.1 -LOOFCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blooum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMY=pto - NORM=ext -HEAPSIZE=500 -MINLEND=0 -MAXIZE=200000000
-USER=USO99474062 @CGN 1 1 3508 @runat 12122003 171322 24931 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQÜERY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPEXT=7
                                                                                                                                                                                                                                          December 13, 2003, 05:17:28; Search time 3730 Seconds (without alignments) 2522.578 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                              - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AC099183 Rattus no
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ALIGNMENTS

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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34752)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alberaia, J., Barke, T., Maratunge, H.C., Akel, R., Ngele, M., Barka, T., Barbaria, J., Barton, P., Briach, C., Blankenburg, K., Bonnin, D., Banch, J., Barton, P., Baryani, D., Banch, P., Burch, P., Burch, P., Burkett, C., Eutrell, K.L., Byrd, N.C., Carron, T.F., Carron, T.F., Chen, Z., Chowdin, D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Deladao, C., Coyle, M.D., Dathorne, S.R., David, R., Deladao, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Daris, C., Coyle, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Harnandez, O., Hodgson, M., Hogues, M., Holloway, C., Hamilton, K., Kara, M., Garcia, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M., Mayara, M
                       AC107303 347572 bp DNA linear HTG 09-MAY-2002 Homo sapiens chromosome 3 clone RP11-595122, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
Submitted (09-MAY-2002) Human Genetics, Baylor College of Medicine, One
E Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this Sequence version replaced gi:18449841.
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Submitted (18-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 347572)
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                      AC107303.3 GI:20335965
HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                     Assembly program: Phrap, version 0.990329
Consensus quality: 331666 bases at least Q40
Consensus quality: 339305 bases at least Q30
Consensus quality: 1400 bases at least Q30
Estimated insert size: 172665; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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Chemistry: Dye-terminator Big Dye: 100%
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Burran, B. Linton, L., Nusbaum, C. and Lander, E. Hominidae, Homo.

Mammalia's Euchrenia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161987)

Birran, B., Linton, L., Nusbaum, C. and Lander, E. Allen, N. Anderson, M. Baker, J., Eachers, C. Colangelo, M. Collins, S. Colangelo, M. Collins, S. Colangelo, M. Collins, S. Collymore, A. Cocke, P. Corliss, D., Depare, E. Devon, K., Dewar, K., Donelan, L., Bertreira, P., FitzHugh, M., Forreat, E., Haaford, A., Herrena, L., Horteria, P., FitzHugh, W. Forreat, S., Haaford, J., Haaford, J., Macdonald, P., Marquis, M., Morris, M., Morrow, J., Wohland, J.C., Jacotoc, L., Jones, C. Kann, L., Morran, R., Maddrin, J., Nolloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Mardis, M., Morris, M., Morrow, J., Wordaman, M., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfayes, S., Tichovolsky, M., Torrealla Miller, I., Volanission

AL Submitted (2e-Vol'1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Shiren, B., Linton, L., Norbaum, C., Lander, E., Allen, N., Anderson, M., Backer, J., Baddwin, J., Barna, N., Beckerly, R., Benn, J., Bowen, A., Cooke, P., Dearellano, K., Depare, S., Collywore, N., Submitsed (2e-Vol'1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Shiren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Backer, J., Baddwin, J., Barna, N., Beckerly, R., Benn, J., Bavan, A., Gage, D., Cadelle, A., Cerry, J., Wardish, J., Barna, N., Beckerly, R., Benn, J., Bears, M., Herena, L., Horton, L., Wendan, M., Calins, S., Collyman, M., McKernan, K., Meldrin, J., Walla, M., Morris, W., Weley, R., Welkernan, K., Meldrin, J., Walla, M., Morris, W., Welley, R., Welkernan, K., Meldrin, J., Walla, M., Werley, R., Welkernan, K., Meldrin, J., Walla, M., Welley, R., Welkernan, K., Welder, W., Wagner, R., Wagner, A., Wagner, A., Wagner, A., Wagner, A., Wagner, A., Wagner, A., Wagner, A., Wagner, A., Wagner, M., Wagner, M., Wag
106036 GTGTCCAGCTGCCGCTGCTTTCAGCTGCCCGACCACCTGCTGTAGAACAACCTGCTTC 106095
                                                                                                                                                                                                                                             PRI 17-DEC-1998
                                                                                                                                                                                                                          AC006070 161987 bp DNA linear PRI 17-DEC-1998
Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence.
AC006070
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The remainder overlaps accession number AC003958 (WICGR project
L295).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-DEC-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 17, 1998 this sequence version replaced gi:4006836. All repeats were identified using RepeatMasker: Smit, A.F.A. &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ArgProSerCysCysIleSerSerCysCysArgProSerCysCysIleSerSerCysCys 60
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     3154 others
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Matches:
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87.83%
87.39%
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                                   195599
210747
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226329
226429
246182
26511
265511
26561
293687
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complement(12319. .12588)
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complement (12942. .13139)
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16556. .16727
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1786_ . 1905

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1569-.1770
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7. .11296
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US-09-874-062-3 (1-230) x AC006070 (1-161987)

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Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139433 GTGTCCAGCTGCCGCTGCCCTTTCAGCTGCCCGACCACCTGCTGTAGAACCTGCTTC 139492
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Rattus norvegicus (Norway rat)
Rattus norvegicus (Sattus norvegicus (Sattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25089200.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecs/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and the feature table. Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Brand, M., Egene, C., Evana, C.A., Falls, T., Fan, G., Fagan, A., Escotto, M., Eugene, C., Evana, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gebregerorgis, E., Geer, K., Gall, R., Garcia, A., Garner, T., Garza, M., Gurrath, M., Guerra, W., Guevara, W., Guaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Hamilton, K., Hannandez, B., Hines, S., Huldw., S.L., Hodgson, A., Hogues, M., Hollins, B., Hollis, S., Huldw., J., Hengues, M., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marpathy, S., Kaelly, S., Khan, Z., Khan, Z., King, L., Kovar, C., Liu, W., Liu, W., Liu, Y., Loulsegd, H., Lozdo, R.J., Lu, X., Ma, J., Mangum, B., Mahindartne, M., Martin, K., Martin, R., Martin, R., Mahindartne, M., Mangum, B., Mahindartne, M., Mangum, B., Mahindartne, M., Martin, K., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Mangum, B., Mapua, P., Martin, R., Mart Submitted (05-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases I to 221952)
Rat Genome Sequencing Consortium. Center: Baylor College of Medicine Center code: BCM ----- Genome Center (bases 1 to 221952)

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AC099183.5 GI:30522049
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                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 1 contigs. Gaps between the contigs.

* are represented as tuns of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* Location/Qualifiers
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                Assembly program: Atlas 3.0; Consensus quality: 213950 bases at least Q40 Consensus quality: 215107 bases at least Q30 Consensus quality: 215809 bases at least Q20 Estimated insert size: 225832; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Matches:
Conservative:
Mismatches:
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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---- Summary Statistics
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To theses I to 25(796)

Muzny, D. Marte., Metxker, M. Lee., Abramzon, S., Adams, C., Alder, J., Algbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Blankenburg, K., Blyth, P., Brown, M., Blayano, K., Blair, D., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Blayano, C., Caver, Blyth, P., Brown, M., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chavazo, D., Chen, G., Chen, R., Chen, G., Chen, R., Chen, G., Coyle, M., Cree, A., D'Souza, D., Davila, M. L., Davis, C., Davoy-Carroll, L., De Anda, C., Dederich, D., Denson, S., Derman, C., Evan, C., Davila, M. L., Davis, C., Dunn, A., Durbin, K., Dudar, C., Berer, K., Egan, A., Escotto, M., Eugene, C., Evan, C., Rand, A., Escotto, M., Eugene, C., Rand, R., Garza, M., Gebregeorgis, E., Geer, K., Gilly, R., Garcia, A., Garrer, M., Gabisi, A., Gabrer, M., Hamil, C., Hamilton, K., Hamilton, K., Harland, W., Hanil, C., Hamilton, C., Hamilton, K., Harlandez, J., Harland, M., Hamil, C., Hamilton, C., Hamilton, K., Johnson, R., Hollins, B., Howells, S., Hladuk, S.L., Hodgson, M., Hernandez, J., Liu, J., Liu, J., Liu, J., Liu, J., Liu, W., Liu, Y., Lohleeged, H., Lorado, R.J., Idebird, D., Jackson, L., Jang, H., Johnson, B., Lopez, J., Liu, J., Liu, W., Liu, Y., Lohleeged, H., Lorado, R.J., Martine, R., Martine, M., Mandartne, R., Martine, S., Mandartie, R., Martine, S., Mandartie, R., Martine, S., Mandartie, R., Martine, S., Mandartie, S., Mandartie, R., Martine, S., Mandartie, R., Martine, S., Mandartie, R., Martine, S., Mandartie, R., Mandan, M., Morris, S., Munidas, R., Peraz, L., Pfannkoch, C., Reall, M., Reiter, M., Reiter, M., Reiter, M., Reith, M., Reith, M., Reith, M., Reith, M., Reith, R., Reith, M., Reith, R., Reith, M., Reith, R., Reith, M., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R., Reith, R.,
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Rattus norvegicus clone CH230-115519, WORKING DRAFT SEQUENCE.
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:23264574.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-seaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs with a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snedty, J., Strong, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Strong, X., Tingey, A., Tabor, P., Taylor, Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Walar, Mang, O., Wang, S., Warren, B., Walker, B., Wang, J., Wallas, S., Warren, T., Walker, B., Wang, J., Williams, G., Willson, R., Walczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, K., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a "working draft' sequence It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One apylor Plaza, Houston, TX 77030, USA (bases 1 to 256796) (Baylor Baylor Plaze) Rat Genome Sequencing Consortium.
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Center project name: GHAG
Center clone name: CH230-115J19
Center clone name: CH230-115J19
Assembly program: Atlas 3.0;
Consensus quality: 222308 bases at least Q40
Consensus quality: 227622 bases at least Q20
Consensus quality: 227746 bases at least Q20
Estimated insert size: 230249; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.Mgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Mismatches:
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complement (252916. .251754)
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clone_end:Spē
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Matches:
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end sequence: BH318731":
255415. .256796
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1. .1534
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clone_end:T7"
19216
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1145.50
78.40%
70.80%
77.19%
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Best Local Similarity:
Query Match:
DB:
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4571 CCCCAGTGCTGTATCTCCCAGTTGCTGCCGCCCGACCTGTTGCGAGACCACTTGCTGCAGA 4512
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                                                                          GlnGluSerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCys 40
                                                                                                                                                         HTG.
Mus musculus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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           MetValSerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly 20
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Mouse DNA sequence from clone RP23-132J20 on chromosome ll,
                                  4511 Accaccretrercecccaecarecreragreerrerrecrec 4470
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ALS90997
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ALD-4EUV4 197658 bp DNA linear HTG 27-FEB-2002 MUS musculus chromosome 11 clone RP23-142E7, *** SEQUENCING IN PROGRESS ***.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 28, 2002 this sequence version replaced gi:18135257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 10876; 100% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Chemistry: Dye-terminator Big Dye; 99% of reads
Consensus quality: 192892 bases at least Q40
Consensus quality: 192997 bases at least Q40
Consensus quality: 192997 bases at least Q40
Consensus quality: 192997 bases at least Q40
Consensus quality: 192997 bases at least Q40
Insert size: 197658; sum-of-contigs
Insert size: 203092; 2.3% error; agarose-fp
Quality coverage: 13.20x in Q20 bases; sum-of-contigs Quality
coverage: 13.17x in Q20 bases; agarose-fp
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HL646094.6 GI:19031714
HTG; HTGS PHASE2; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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42073 c 41216 g 55162 t
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/clone="RP23-142B7"
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Web site: http://www.sanger.ac.uk
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1131.50
67.69%
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76.25%
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Direct Submission
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Best Local Similarity:
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            Blakey, S.

Direct Submission

AL Submitted (12-1001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries:

Direct Submission

Cambridgeshire, CB10 15A, UK. B-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 30, 2001 this sequence version replaced gi:16979523.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, curectory or the contraction or plasmic submit with their source databases: Em:, EMBL; SW:, curectory or the contraction or plasmic subcontraction or plasmic such as contraction were contraction or the contraction or plasmic such as contraction or plasmic such the sequence of the sequence or the contraction or plasmic such the following and the plane are used to associate primary accession numbers given the contraction or plasmic such the sequence or the contraction or plasmic such the sequence or the contraction or plasmic such the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Tandem repeat. Forced join. Gap size estimated to
be approximately 260bp by restriction digest data."
115669, .115073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transposon (V0061) removed here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-132J20 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP23-132J20 The true left end of clone RP23-212C14 is at 95441 in this sequence. The true right end of clone RP23-272C1 is at 89011 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Sequence from overlapping clone RP23-212C14 (AL590992). Assembly confirmed by restriction digest."
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/note="1327 bases of IS2 transposon (V00
Flanking repeat sequences are irregular.
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Matches:
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="11"
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/clone_lib="RPCI-23"
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     (bases 1 to 200602)
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67.69%
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76.25%
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Best Local Similarity:
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Pred. No.:
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161661 CCTTCCTGCTGCCGCCCTAGCTGCTGTGTCCAGCTGCTGCAGGCCCTCTTGCTGCTGCATC 161602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 ThrThrCysCysArgProSerCysIleSerSerCysTyrArgPro----- 177
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrThrCysPheHisProIleCysCysGlySerSerCysCys 230
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Submitted (29-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 30, 2001 this sequence version replaced gi:1697923.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-etranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL: Sw:,
SWISSPROT; Tr:, TREMBL: Wp:, WORMPEP: Information on the WORMPEP
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                                                                                                                                                                                                                                                                                     ProSerCysCysArgProAlaCysCysIleSerSerCysCysHisProSerCysCysVal 201
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Sciurognathi; Muridae; Murinae; Mus
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from the RPCI-23 Mouse PAC Library
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                                                                                          ---SerCysCysArgProSerCysCysIeSerSerCysCysLysProSerCysCysGln
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Mouse DNA sequence from clone RP23-132J20 on chromosome ll,
---SerCysCysArgThrThrCysCysArgProSerCysCysIleSer
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/mol_type="genomic DNA"
/db xref="taxon:10090"
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 200602)
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Direct Submission
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                                                                                                                      Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assequencing vector: plasmid; 10875; 99% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Consensus quality: 19282 bases at least 040
Consensus quality: 19297 bases at least 040
Consensus quality: 193039 bases at least 020
Insert size: 197658; sum-of-contigs
Insert size: 203092; 2.3% error; agarose-fp
Quality coverage: 13.20x in Q20 bases; sum-of-contigs Quality
coverage: 13.17x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

Location/Qualifiers
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly fragment:02832"
42073 c 41216 g 55162 t
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                                                                                ------ Project Information
                                site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="11"
/clone="RP23-142E7"
                                                                                                    Center project name: bM142E7
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Best Local Similarity:
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Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
Con Mar 21, 2002 this sequence version replaced gi:18873624.

During sequence assembly data is compared from overlapping clones mancation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWESSROT; TT:, TREMBL; WP:, WORMBEP: Information on the WORMBEP.
ALS90992 118444 bp DNA linear ROD 14-MAR-2002
Mouse DNA sequence from clone RP23-212C14 on chromosome 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-212C14 is from the RPC1-31 Mouse PAC Library
constructed by the group of Pieter de Jong.
constructed by the group of Pieter de Jong.
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP23-212C14 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RP23-212C14 is at 118444 in this sequence. The true right end of clone RP23-212C14 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 118444)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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25469 c 24703 g 32390
                                                                   ProlleCysCysGlySerSerCysCys 230

    .118444
    /organism="Mus musculus"

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/db_xref="taxon:10090"
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/clone="RP23-212C14"
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                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
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1006.50
76.52$
66.96$
67.82$
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Best Local Similarity:
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Pred. No.:
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerCysCysLysProSerCysCysArgThrThrCysCysArgProSerCysCysIle 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SerCysCysArgProSerCysCysIleSerSerCysCysLysProSerCysCysGln 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerCy8ArgCy8ProPheSerCy8ProThrThrCy8Cy8ArgThrThrCy8PheHis 221
                                                                                          /note="Tandem repeat. Forced join. Gap size estimated to
be approximately 260bp by restriction digest data."
115669. 11570. /note="1327 bases of IS2 transposon (V0061) removed here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnGluSerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCys 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ArgProSerCysCysIleSerSerCysCysArgProSerCysCysIleSerSerCysCys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LysProSerCysCeuThr------ThrCysCysArgThrThrCysCys 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetValSerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly 20
                                                                                                                                                                                                                     /note="Sequence from overlapping clone RP23-212C14 (AL590992). Assembly confirmed by restriction digest." 188825. .188863
                                                                                                                                                                                                                                                                                               /note="Sequence from uni-directional dGTP big dye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SerCysCysArgThrThrCysCysArgProSerCysCysIleSer---
                                                                                                                                                                                    Flanking repeat sequences are irregular.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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40464 c 42904 g 58804 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-874-062-3 (1-230) x AL590997 (1-200602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
    /chromosome="11"
/clone="RP23-132J20"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                               3.91e-32
1110.00
77.91%
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Best Local Similarity:
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Center project name: MCCE
Center project name: RP23-326H14
Center clone name: RP23-326H14
Center clone name: RP23-326H14
Sequencing vector: M13, L08816
Sequencing vector: M13, L08816
Chemistry: Dye-primer Bodipy: 57% of reads
Chemistry: Dye-terminator Big Dye: 43% of reads
Chemistry: Dye-terminator Big Dye: 43% of reads
Chemistry: Dye-terminator Big Dye: 43% of reads
Consensus quality: 19575 bases at least Q40
Consensus quality: 191575 bases at least Q30
Consensus quality: 192401 bases at least Q30
Consensus quality: 192401 bases at least Q30
Consensus quality: 020 bases; agarose-fp estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 7.8x in Q20 bases; sum-of-contigs estimation
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B., Peraz,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Direct Submission

L Unpublished

L Unpublished

L Obase 1 to 192027)

S Worley,K.C.

Morley,K.C.

Morley,K.C.

L Submitted (27-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaze, Houston, TX 77030, USA

On Jan 4, 2001 this sequence version replaced gi:11192108.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71311: contig of 71311 bp in length
71411: gap of unknown length
116268: contig of 44857 bp in length
116368: gap of unknown length
144312: contig of 28944 bp in length
144312: gap of unknown length
173610: contig of 28198 bp in length
173610: contig of 28198 bp in length
173710: gap of unknown length
190868: gap of unknown length
190868: gap of unknown length
192027: contig of 1059 bp in length
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155
16
24
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Contact: hgsc-help@bcm.tmc.edu
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/db_xref="taxon:10090"
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E 1 (bases 1 to 192027)

Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Buhay,C., Burset,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Hobak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,S., Kovar,C., Liu,W., Lollseged,H., Lozado,R.J., Marrin,R., Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
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                                                                                    6214 ATGGTCAGCTCCTGTTGTGGCTCTTGTGTGTGGGCTGTGGCCAAGGC-----
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION

RESULT 10

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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klain, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Minenga, V., Morrow, J., Wurphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, E., Spencer, B., Stange-Thomann, N., Schauer, S., Severy, P., Spencer, B., Velance, J., Vessiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalnoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W. J., Young, G., Zalnoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 1, 2000 this sequence version replaced gi:7249428.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 172432; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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gap of 100 bp
contig of 3777 bp in length
gap of 100 bp
contig of 2281 bp in length
gap of 100 bp
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100 bp
of 6226 bp in length
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contig of 7419 bp in length
gap of 100 bp
contig of 8269 bp in length
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                                                             33905 -----TGCTGCCAGCCCAGCTGCTGCCAGACCACCTGCTAGAACCACCTGCTAGCTGC 33955
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Homo sapiens clone RPl1-585G19, WORKING DRAFT SEQUENCE, 17
unordered pieces.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                               61 LysProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCys 80
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                                       1 MetValSerSerCysCysGySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly
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Unpublished
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Homo sapiens (human)
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/clone lib="RPCI-11 Human Male BAC"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 34752)

1 (Dases) Lo. 34752)

Sis Muzny, D.M.; Adams, C., Adio-Oduola, B., Ali-Osman, F.R.; Allen, C., Alabrooks; S.L.; Amaratunge, H.C.; Are, J.R.; Ayele, M.; Banks, T.; Barbaria, J.; Benton, J.; Bimage, K.; Blankenburg, K.; Bonnin, D.; Bouck, J.; Bowie, S.; Brieva, M.; Brown, M.; Bryant, N.P.; Bubay, C.; Burch, P.; Burkett, C.; Burch, E.; Brown, M.; Bryant, N.P.; Chen, G.; Chen, R.; Chen, Z.; Chowdhry, I.; Charistopoulos, C.; Chen, R.; Chen, Z.; Chowdhry, I.; Christopoulos, C.; Coyle, M.D.; Dathorne, S.R.; David, R.; David, M.; David, M.; David, C.; Day-Carroll, L.; Dederich, D.A.; Douthwaite, K.S.; Dapar, C.; Coyle, M.D.; Ding, Y.; Dinh, H.H.; Douthwaite, K.S.; Dagards, C.C.; Elhaj, C.; Bacotto, M.; Earnhart, C.; Edgar, D.; Ganrell, J.; Foster, P.; Frantz, P.; Gabisi, A.; Gao, J.; Garcia, A.; Ganrer, T.; Garza, N.; Gill, R.; Guevara, W.; Gunaratne, P.; Haniton, K.; Harris, C.; Harris, K.; Hart, M.; Havlak, P.; Hawes, A.; Hernandez, J.; Harris, K.; Hart, M.; Holloway, C.; Hollins, B.;
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Homo sapiens chromosome 3 clone RP11-595122, WORKING DRAFT
SEQUENCE, 32 unordered pieces.
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ACI07303.3 GI:20335965
HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO SADIENS (Numan)
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsoon, E., Khan, U., King, L., Korvah, J., Kovar, C., Kratlsoon, E., Khan, U., King, L., Korvah, J., Kovar, C., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulseged, H., Lozado, R.J., Lui, K., Luda, R., Man, J., Mahsebwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meddor, M., Mai, G., Metzker, Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Okwoon, G., Oguh, M., Okwoon, G., Newtson, M., Nickerson, E., Nwoksen, W., Okwoon, G., Oraumye, N., Oviedo, R., Parce, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rhoeshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Stott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, B., Thomas, N., Thomas, S., Umans, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Walliamson, A., Washington, C., Walliamson, A., Washington, C., Walliamson, S., Warter, R., Washington, C., Walliamson, S., Warter, R., Washington, C., Walliamson, Direct Submission

All Unpublished
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NOTE: This is a "working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
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Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
Submitted (109-MAY-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:18449841.

Center: Baylor College of Medicine
Center Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: RP11-595122
------ Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 331666 bases at least Q40
Consensus quality: 341440 bases at least Q30
Consensus quality: 172965; sum-of-contigs estimation
Gullity coverage: 5x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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                                                                        311249 CAACCCACTGCTGTCGCCCCAGCTGTGAGACGACCTGCTGCCACCTAGGTGCTGC 311190
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Rattus norvegicus clone CH230-166D21, WORKING DRAFT SEQUENCE.
ACU98902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ------CyslleSerSerCysTyrArgProGlnCysCysGlnProSerCysCys 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgProAlaCysCysIleSerSerCysCys------HisPro 197
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                         MetValSerSerCysCysGlySerValCysSerAspGlnSerCysGlyGlnGlyLeuGly 20
                                                                                                                                        GlnGluSerCysCysArgProSerCysCysGlnThrThrCysCysArgThrThrCysCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ThrCysCysArgProSerCysCysIleSerSerCysCysArgProSerCysCys
                                                                                                                                                                                                                             61 LysProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCys
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
US-09-874-062-3 (1-230) x AC107303 (1-347572)
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May 10, 2003 Human Geneme Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 Huis sequence version replaced gi:25089200. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tuc.edu/projects/rat/). Each contrig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Deneon, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drapan-Rocha, S., Dunn, A., Dutchin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Farser, C. M., Garta, M., Garta, A., Garta, A., Garta, M., Garta, M., Gebregorgis, E., Geer, K., Gall, R., Garda, A., Garta, M., Guerara, W., Guerara, W., Guerara, W., Guerara, W., Guerara, W., Guerara, M., Ganta, E., Handen, S.L., Hanglton, C., Hamilton, K., Hanles, P., Haaland, R., Handlton, C., Hamilton, K., Hanles, S., Hilbe, S., Hund, J., Idlehird, D., Jackson, A., Hodles, C., Kardt, C., Jang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Liu, Y., Liu, M., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Louged, H., Lougeged, H., Lozado, R.J., Lewis, L., Li, Z., Liu, J., Liu, M., Liu, Y., Lu, M., Mahindathne, M., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., W
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Direct Submission
Submitted (105-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 221952)
Rat Genome Sequencing Consortium.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Project Information

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221 HisprolleCysCysGlySerSerCysCys 230
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/db_xref="taxon:9606"
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                                                                                                                                                                      (see http://www.hggc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 221952: contig of 221952 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LysProSerCysCysLeuThrThrCysCysArgThrThrCysCysArgProSerCysCys 80
             Center clone name: CH210-166D21
------- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 213950 bases at least Q40
Consensus quality: 215107 bases at least Q30
Consensus quality: 215809 bases at least Q30
Estimated insert size: 225832; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #8805 CAGCCCACCTGTTGCAGGCCTACCTGTTGCCGTCCCAGCTGTTGCCCCAGCTGCTGT
                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
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Matches:
Conservative:
Mismatches:
Indels:
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47344 c 43902 g 61410 t
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                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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/clone="CH230-166D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="clone_boundary
Center project name: GINS
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site:EcoRI
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73.91%
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/protein_id="CAC27578.1"

/db_xref="da1:12655452"

/db_xref="da1:12655452"

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VCCQPTCGHPSCCISSCCRPSCCSSCCRPSCCSSCCRPSCCSSCCRPSCCS

ESSSCCRPCCCRPCCCLRPVGGRVSCHTTCYRPTCVISTCPRPLCCASSCC"

1127. 11132

/gene="KRTAP4.7"
                                                                                                                                                              48550 CGC---CCCTGCTGTGGTAGTTCCAGCTGTGGATCTAGCTGCTGCTGCCCCCCAGCTGCTGT 48494
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Homo sapiens mRNA for keratin associated protein 4.7 (KRTAP4.7
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Submitted (16-OCT-2000) Rogers M.A., Research Program B, German
Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg,
Germany 69120, GERWANY
Related genomic sequence: AC025904 (142457-143089nt, neg strand).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
48610 ATCTCTAGCTGCTGCCGCCCTTCTGTTGCATTTCTAGCTGCTGCAGGCCTTCTTGCTGC
                                                                                         161 GlnThrThrCysCysArgProSerCysCysIleSerSerCysTyrArgProGlnCysCys
                                                                                                                                                                                                                                                                                                                                                               201 ValSerSerCysArgCysProPheSerCysProThrThrCysCysArgThrThrCysPhe
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AJ406939.1 GI:12655451
Keratin associated protein 4.7; KRTAP4.7 gene.
Homo sapiens
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TITLE
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AUTHORS
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 17, clone RP11-619M15
                                                                                                                                                                                                         41 ArgProSerCyaCys1leSerSerCyaCyaRagProSerCyaCys1leSerSerCyaCys 60
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Homo sapiens chromosome 17, clone RP11-619M15, complete sequence.
AC037482
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347 CAGTCTGTGCTGCCAGCCCAGCTGCTGCCAGCTGCTGCTCCAGCTGCTGT
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Matches:
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Homo sapiens
                                  977.00
74.25%
66.95%
65.84%
                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                Alignment Scores:
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B Birren, B. Lintcon, L. Nuabauu, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baidden, J., Barria, N., Bastren, V., Baidden, J., Baidden, J., Barria, N., Bastren, V., Baidden, J., Gabtel, P., Baidden, J., Baidden, J., Barria, N., Bastren, V., Baidden, J., Gabtel, J., Baidden, J., Baidden, J., Barria, N., Barten, N., Barten, C., Barria, N., Bogula, M., Castrel, A., Castrel, A., Chopepo, D., Gargod, B., Barria, N., Barten, V., Barten, V., Barten, N., Barten, C., Barten, N., Barten, C., Barten, C., Brown, A., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C., Barten, C.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 23, 2002 this sequence version replaced gi:18693527.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                    Only the first 186.1 kilobases of this clone are being submitted.
The remainder overlaps accession number AC004231 (WICGR project
L297].
                                                                                                                                                     ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L9334
Center clone name: 619_M 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11 Human Male BAC"
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complement(314. .642)
/rpt family="L1MC5"
complement(314. .642)
/rpt family="L1MC5"
/rpt family="L1MC5"
/rpt family="L1MC4"
                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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omplement(6526. .6560)
note="single clone coverage"
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8562. .8751
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complement (1504. 1585)
/rpt_family="LiMA9"
complement (1707. 2219)
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complement (2278. 2566)
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/mol_type="genomic DNA"
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/rpt_family="AT_rich"
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/rpt_family="MIR"
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rpt_family="L1PA8"
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omplement (7231. .7419)
rpt family="L1PA5"
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